

Bulk RNA-seq

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 An abbreviated version of this protocol was published in Science in Oct 2020

Gene regulatory networks controlling vertebrate retinal regeneration

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Detailed protocol

Flow-sorted RNA samples were sent for library preparation and sequencing. Briefly, ribosomal RNA was depleted, and total RNA was captured from the RNA samples using Illumina TruSeq Stranded RNA LT kit Ribo-Zero Gold (#15032619, Illumina). Around 8 to 10 libraries were pooled and sequenced for paired-end 75 cycles using the NextSeq 500 system with ~400 million to 500 million reads per run, resulting in between ~45 million and 55 million reads per library.

How to cite: (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Hoang, T. , Wang, J. , Hyde, D. , Qian, J. , Blackshaw, S. and Boyd, P. (2022). Bulk RNA-seq. Bio-protocol Preprint. bio-protocol.org/prep1778.
2. Hoang, T., Wang, J., Boyd, P., Wang, F., Santiago, C., Jiang, L., Yoo, S., Lahne, M., Todd, L. J., Jia, M., Saez, C., Keuthan, C., Palazzo, I., Squires, N., Campbell, W. A., Rajaii, F., Parayil, T., Trinh, V., Kim, D. W., Wang, G., Campbell, L. J., Ash, J., Fischer, A. J., Hyde, D. R., Qian, J. and Blackshaw, S.(2020). Gene regulatory networks controlling vertebrate retinal regeneration. Science. DOI: [10.1126/science.abb8598](https://doi.org/10.1126/science.abb8598)

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